

#2



ENTERED OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,913

DATE: 03/19/2002
TIME: 14:49:54

Input Set : A:\#373819 v1 - 33474-PCT-USA-A Sequence Listing.txt
Output Set: N:\CRF3\03192002\J086913.raw

4 <110> APPLICANT: Higuchi, Maria de Lourdes
5 Schenkman, Sergio
7 <120> TITLE OF INVENTION: PREVENTION AND TREATMENT OF
8 MYCOPLASMA-ASSOCIATED DISEASES
10 <130> FILE REFERENCE: 33474-PCT-USA-A 068528.0103
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/086,913
C--> 13 <141> CURRENT FILING DATE: 2002-03-01
15 <150> PRIOR APPLICATION NUMBER: PCT/BR01/00083
16 <151> PRIOR FILING DATE: 2001-03-07
18 <150> PRIOR APPLICATION NUMBER: Not Yet Assigned
19 <151> PRIOR FILING DATE: 2001-03-07
21 <150> PRIOR APPLICATION NUMBER: PI 0002989-0 BR
22 <151> PRIOR FILING DATE: 2000-03-07
24 <160> NUMBER OF SEQ ID NOS: 4
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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29 <211> LENGTH: 2010
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Variant of T. Cruzi trans-sialidase gene
36 <400> SEQUENCE: 1
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38 atggcaccgc gatcgagcgc agttgagctg tttaagcggc aaagctcgaa ggtgccattt 120
39 gaaaaggcgc gcaaagtcac cgagcggggt gtccactcgt tccgcctccc cgcccttggt 180
40 aatgtggacg ggggtgatgt tgccatcgcg gacgctcgct acgaaacatc caatgacaac 240
41 tccctcattg atacggtggc gaagtacagc gtggacgatg gggagacgtg ggagacccaa 300
42 attgccatca agaacagtcg tgcctcgtct gtttctcgtg tgggtggatcc cacagtgtat 360
43 gtgaagggca acaagcttta cgtcctgggt ggaagctaca acagttcgag gagctactgg 420
44 acgtcgcatg gtgatgcgag agactgggat attctgcttg ccgttggtga ggtcacgaag 480
45 tccactgcgc gcggcaagat aactgcgagt atcaaattgg ggagccccgt gtcactgaag 540
46 gaatttttcc cggcggaat ggaaggaatg cacacaaatc aatttcttgg cgggtgcaggt 600
47 gttgccattg tggcgtccaa cgggaatctt gtgtaccctg tgcaggttac gaacaaaaag 660
48 aagcaagttt tttccaagat cttctactcg gaagacgagg gcaagacgtg gaagtttggg 720
49 gagggtagga gtgattttgg ctgctctgaa cctgtggccc ttgagtggga ggggaagctc 780
50 atcataaaca ctcgagtga ctatcgccgc cgtctggtgt acgagtccag tgacatgggg 840
51 aattcgtggg tggaggctgt cggcacgctc tcacgtgtgt gggggccctc accaaaatcg 900
52 aaccagcccgc gcagtcagag cagcttcaact gccgtgacca tcgaggggaat gcgtgttatg 960
53 ctcttcacac acccgctgaa ttttaaggga aggtggctgc gcgaccgact gaacctctgg 1020
54 ctgacggata accagcgcac ttataacggt gggcaagtat ccattggtga tgaaaattcc 1080
55 gcctacagct ccgtcctgta caaggatgat aagctgtact gtttgcatga gatcaacagt 1140
56 aacgaggtgt acagccttgt ttttgcgcg cgtggttggc agctacggat cattaatatca 1200
57 gtgctgcagt cctggaagaa ttgggacagc cacctgtcca gcatttgcac ccctgctgat 1260

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58 ccagccgctt cgtcgtcaga gcgtggttgt ggtcccgtg tcaccacggt tggctctgtt 1320
59 ggctttttgt cgcacagtgc caccaaaacc gaatgggagg atgctgaccg ctgctgcaac 1380
60 gcaagcacgg caaatgcgga gaggggttccg aacggtttga agtttgccgg ggttgccgga 1440
61 ggggcgcttt ggccggtgag ccagcagggg cagaatcaac ggtatcactt tgcaaaccac 1500
62 gcgttcacgc tgggtggcgtc ggtgacgatt cagcaggttc cgagcgtcgc gagtcccttg 1560
63 ctgggtgcga gcctggactc ttctggtggc aaaaaactcc tggggctctc gtacgacgag 1620
64 aagcaccagt ggcagccaat atacggatca acgccggtga cgccgaccgg atcgtgggag 1680
65 atgggtaaga ggtaccagt ggttcttacg atggcgaata aaattggttc ggtgtacatt 1740
66 gatggagaac ctctggaggg ttcagggcag accggtgtgc cagacgggag gacgcctgac 1800
67 atctccact tctacgttgg cgggtatgga aggagtata tgccaacat aagccactg 1860
68 acggtgaata atgttcttct ttacaaccgt cagctgaatg ccgaggagat caggacctg 1920
69 ttcttgagcc aggacctgat tggcacggaa gcacacatgg gcagcagcag cggcagcagt 1980
70 gaaagaagta cgcccgatc cggtgctaa                                2010

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72 <210> SEQ ID NO: 2

73 <211> LENGTH: 669

74 <212> TYPE: PRT

75 <213> ORGANISM: Artificial Sequence

77 <220> FEATURE:

78 <223> OTHER INFORMATION: Variant of T. Cruzi trans-sialidase protein

80 <400> SEQUENCE: 2

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81 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
82 1 5 10 15
83 Arg Gly Ser His Met Ala Pro Gly Ser Ser Arg Val Glu Leu Phe Lys
84 20 25 30
85 Arg Gln Ser Ser Lys Val Pro Phe Glu Lys Gly Gly Lys Val Thr Glu
86 35 40 45
87 Arg Val Val His Ser Phe Arg Leu Pro Ala Leu Val Asn Val Asp Gly
88 50 55 60
89 Val Met Val Ala Ile Ala Asp Ala Arg Tyr Glu Thr Ser Asn Asp Asn
90 65 70 75 80
91 Ser Leu Ile Asp Thr Val Ala Lys Tyr Ser Val Asp Asp Gly Glu Thr
92 85 90 95
93 Trp Glu Thr Gln Ile Ala Ile Lys Asn Ser Arg Ala Ser Ser Val Ser
94 100 105 110
95 Arg Val Val Asp Pro Thr Val Ile Val Lys Gly Asn Lys Leu Tyr Val
96 115 120 125
97 Leu Val Gly Ser Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly
98 130 135 140
99 Asp Ala Arg Asp Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys
100 145 150 155 160
101 Ser Thr Ala Gly Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro
102 165 170 175
103 Val Ser Leu Lys Glu Phe Phe Pro Ala Glu Met Glu Gly Met His Thr
104 180 185 190
105 Asn Gln Phe Leu Gly Gly Ala Gly Val Ala Ile Val Ala Ser Asn Gly
106 195 200 205
107 Asn Leu Val Tyr Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe
108 210 215 220
109 Ser Lys Ile Phe Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 110 | 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| 111 | Glu | Gly | Arg | Ser | Asp | Phe | Gly | Cys | Ser | Glu | Pro | Val | Ala | Leu | Glu | Trp |
| 112 | | | | | 245 | | | | | 250 | | | | | 255 | |
| 113 | Glu | Gly | Lys | Leu | Ile | Ile | Asn | Thr | Arg | Val | Asp | Tyr | Arg | Arg | Arg | Leu |
| 114 | | | | 260 | | | | | 265 | | | | | | 270 | |
| 115 | Val | Tyr | Glu | Ser | Ser | Asp | Met | Gly | Asn | Ser | Trp | Val | Glu | Ala | Val | Gly |
| 116 | | | 275 | | | | | 280 | | | | | 285 | | | |
| 117 | Thr | Leu | Ser | Arg | Val | Trp | Gly | Pro | Ser | Pro | Lys | Ser | Asn | Gln | Pro | Gly |
| 118 | | 290 | | | | | 295 | | | | | 300 | | | | |
| 119 | Ser | Gln | Ser | Ser | Phe | Thr | Ala | Val | Thr | Ile | Glu | Gly | Met | Arg | Val | Met |
| 120 | 305 | | | | | 310 | | | | 315 | | | | | | 320 |
| 121 | Leu | Phe | Thr | His | Pro | Leu | Asn | Phe | Lys | Gly | Arg | Trp | Leu | Arg | Asp | Arg |
| 122 | | | | 325 | | | | | | 330 | | | | | 335 | |
| 123 | Leu | Asn | Leu | Trp | Leu | Thr | Asp | Asn | Gln | Arg | Ile | Tyr | Asn | Val | Gly | Gln |
| 124 | | | | 340 | | | | | 345 | | | | | 350 | | |
| 125 | Val | Ser | Ile | Gly | Asp | Glu | Asn | Ser | Ala | Tyr | Ser | Ser | Val | Leu | Tyr | Lys |
| 126 | | | 355 | | | | | 360 | | | | | 365 | | | |
| 127 | Asp | Asp | Lys | Leu | Tyr | Cys | Leu | His | Glu | Ile | Asn | Ser | Asn | Glu | Val | Tyr |
| 128 | | 370 | | | | | 375 | | | | | 380 | | | | |
| 129 | Ser | Leu | Val | Phe | Ala | Arg | Leu | Val | Gly | Glu | Leu | Arg | Ile | Ile | Lys | Ser |
| 130 | 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| 131 | Val | Leu | Gln | Ser | Trp | Lys | Asn | Trp | Asp | Ser | His | Leu | Ser | Ser | Ile | Cys |
| 132 | | | | 405 | | | | | | 410 | | | | | 415 | |
| 133 | Thr | Pro | Ala | Asp | Pro | Ala | Ala | Ser | Ser | Ser | Glu | Arg | Gly | Cys | Gly | Pro |
| 134 | | | 420 | | | | | | 425 | | | | | 430 | | |
| 135 | Ala | Val | Thr | Thr | Val | Gly | Leu | Val | Gly | Phe | Leu | Ser | His | Ser | Ala | Thr |
| 136 | | | 435 | | | | | 440 | | | | | 445 | | | |
| 137 | Lys | Thr | Glu | Trp | Glu | Asp | Ala | Tyr | Arg | Cys | Val | Asn | Ala | Ser | Thr | Ala |
| 138 | | 450 | | | | | 455 | | | | | 460 | | | | |
| 139 | Asn | Ala | Glu | Arg | Val | Pro | Asn | Gly | Leu | Lys | Phe | Ala | Gly | Val | Gly | Gly |
| 140 | 465 | | | | | 470 | | | | | 475 | | | | 480 | |
| 141 | Gly | Ala | Leu | Trp | Pro | Val | Ser | Gln | Gln | Gly | Gln | Asn | Gln | Arg | Tyr | His |
| 142 | | | | 485 | | | | | | 490 | | | | | 495 | |
| 143 | Phe | Ala | Asn | His | Ala | Phe | Thr | Leu | Val | Ala | Ser | Val | Thr | Ile | His | Glu |
| 144 | | | | 500 | | | | | 505 | | | | | 510 | | |
| 145 | Val | Pro | Ser | Val | Ala | Ser | Pro | Leu | Leu | Gly | Ala | Ser | Leu | Asp | Ser | Ser |
| 146 | | | 515 | | | | | 520 | | | | | 525 | | | |
| 147 | Gly | Gly | Lys | Lys | Leu | Leu | Gly | Leu | Ser | Tyr | Asp | Glu | Lys | His | Gln | Trp |
| 148 | | 530 | | | | | 535 | | | | | 540 | | | | |
| 149 | Gln | Pro | Ile | Tyr | Gly | Ser | Thr | Pro | Val | Thr | Pro | Thr | Gly | Ser | Trp | Glu |
| 150 | 545 | | | | | 550 | | | | | 555 | | | | 560 | |
| 151 | Met | Gly | Lys | Arg | Tyr | His | Val | Val | Leu | Thr | Met | Ala | Asn | Lys | Ile | Gly |
| 152 | | | | 565 | | | | | | 570 | | | | | 575 | |
| 153 | Ser | Val | Tyr | Ile | Asp | Gly | Glu | Pro | Leu | Glu | Gly | Ser | Gly | Gln | Thr | Val |
| 154 | | | | 580 | | | | | 585 | | | | | 590 | | |
| 155 | Val | Pro | Asp | Gly | Arg | Thr | Pro | Asp | Ile | Ser | His | Phe | Tyr | Val | Gly | Gly |
| 156 | | | 595 | | | | | 600 | | | | | 605 | | | |
| 157 | Tyr | Gly | Arg | Ser | Asp | Met | Pro | Thr | Ile | Ser | His | Val | Thr | Val | Asn | Asn |
| 158 | | 610 | | | | | 615 | | | | | 620 | | | | |

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159 Val Leu Leu Tyr Asn Arg Gln Leu Asn Ala Glu Glu Ile Arg Thr Leu
 160 625 630 635 640
 161 Phe Leu Ser Gln Asp Leu Ile Gly Thr Glu Ala His Met Gly Ser Ser
 162 645 650 655
 163 Ser Gly Ser Ser Glu Arg Ser Thr Pro Gly Ser Gly Cys
 164 660 665

167 <210> SEQ ID NO: 3

168 <211> LENGTH: 28

169 <212> TYPE: DNA

170 <213> ORGANISM: Artificial Sequence

172 <220> FEATURE:

173 <223> OTHER INFORMATION: Trans-sialidase gene primer

175 <400> SEQUENCE: 3

176 ggaattccat atggcacccg gatcgagc

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178 <210> SEQ ID NO: 4

179 <211> LENGTH: 34

180 <212> TYPE: DNA

181 <213> ORGANISM: Artificial Sequence

183 <220> FEATURE:

184 <223> OTHER INFORMATION: Trans-sialidase gene primer

186 <400> SEQUENCE: 4

187 cggatccggg cgtacttctt tcactggtgc cggt

34

VERIFICATION SUMMARY

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Input Set : A:\#373819 v1 - 33474-PCT-USA-A Sequence Listing.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date